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Amendments to the Claims

Claims 1-485 (Canceled)

486.   (Currently Amended)   A method for determining whether one or more non-viral target species may be present in a sample, said method comprising the steps of:

a)   contacting said sample with hybridization assay means for detecting the presence of a nucleic acid variable region characteristic of nucleic acid of said one or more target species, wherein said means distinguishes said variable region from nucleic acid of at least one non-target species, wherein said variable region is present in an rRNA sequence, or a DNA sequence encoding for said rRNA sequence, in a location corresponding to a target region selected from the group consisting of:

bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;

bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;

bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;

bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;

bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;

bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;

bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;

bases ~~980-1060~~ 975-1060 of E. *coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;

bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA;

bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;

bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;

bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;

bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA;

bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and

bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA,

provided that if said one or more target species include at least one species of *Mycoplasma*, then said target region is in a location corresponding to bases 65-108, 190-230, 450-490, 820-860 or 1255-1290 of *E. coli* 16S rRNA or the encoding DNA, and

provided that if said target region is present in a location corresponding to bases ~~1250-1290~~ 1255-1290 of *E. coli* 16S rRNA, or the encoding DNA, then said one or more target species is *Mycoplasma pneumoniae* and said at least one non-target species includes a *Mycoplasma* species other than *Mycoplasma pneumoniae*; and

b)   determining whether said means has detected the presence of said variable region as an indication that at least one member of said one or more target species is present in said sample.

487.   (Currently Amended) A method for determining whether one or more non-viral target species may be present in a sample, said method comprising the steps of:

a)   contacting said sample with an oligonucleotide probe which distinguishes between nucleic acid of said one or more target species from nucleic acid of at least one non-target species, wherein a duplex formed between said oligonucleotide probe and a variable region present in nucleic acid of said one or more target species has a higher Tm than a duplex formed between said oligonucleotide probe and said variable region present in nucleic acid of said at least one non-target species, wherein said variable region is present in an rRNA sequence, or a DNA sequence encoding for said rRNA sequence, in a location corresponding to a target region selected from the group consisting of:

bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;

bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;

bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;

bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;

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bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;

bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;

bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;

bases ~~980-1060~~ 975-1060 of *E. coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;

bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA;

bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;

bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;

bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;

bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA;

bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and

bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA,

provided that if said one or more target species include at least one species of *Mycoplasma*, then said target region is in a location corresponding to bases 65-108, 190-230, 450-490, 820-860 or 1255-1290 of *E. coli* 16S rRNA or the encoding DNA, and

provided that if said target region is ~~present~~ in a location corresponding to bases ~~1250-1290~~ 1255-1290 of *E. coli* 16S rRNA, or the encoding DNA, then said one or more target species is *Mycoplasma pneumoniae* and said at least one non-target species includes a *Mycoplasma* species other than *Mycoplasma pneumoniae*; and

b)   determining whether a nucleic acid complex comprising said oligonucleotide probe has formed under conditions of high stringency as an indication that at least one member of said one or more target species is present in said sample, wherein said oligonucleotide probe does not form a detectable duplex with nucleic acid of said at least one non-target species under said conditions.

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488. (Currently Amended) A method for determining whether one or more non-viral target species may be present in a sample, said method comprising the steps of:

a) contacting said sample with hybridization assay means for detecting the presence of a nucleic acid variable region characteristic of nucleic acid of said one or more target species, wherein said means distinguishes said variable region from nucleic acid of at least one non-target species belonging to the same genus as said one or more target species, wherein said variable region is present in an rRNA sequence, or a DNA sequence encoding for said rRNA sequence, in a location corresponding to a target region selected from the group consisting of:

bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;

bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;

bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;

bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;

bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;

bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;

bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;

bases ~~980-1060~~ 975-1060 of *E. coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;

bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA;

bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;

bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;

bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;

bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA;

bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and

bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA,

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provided that if said target region is ~~present~~ in a location corresponding to bases ~~1250-1290~~ 1255-1290 of *E. coli* 16S rRNA, or the encoding DNA, then said one or more target species is *Mycoplasma pneumoniae*; and

b) determining whether said means has detected the presence of said variable region as an indication that at least one member of said one or more target species is present in said sample.

489. (Currently Amended) A method for determining whether one or more non-viral target species may be present in a sample, said method comprising the steps of:

a) contacting said sample with an oligonucleotide probe which distinguishes between nucleic acid of said one or more target species from nucleic acid of at least one non-target species belonging to the same genus as said one or more target species, wherein a duplex formed between said oligonucleotide probe and a variable region present in nucleic acid of said one or more target species has a higher Tm than a duplex formed between said oligonucleotide probe and said variable region present in nucleic acid of said at least one non-target species, wherein said variable region is present in an rRNA sequence, or a DNA sequence encoding for said rRNA sequence, in a location corresponding to a target region selected from the group consisting of:

bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;

bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;

bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;

bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;

bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;

bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;

bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;

bases ~~980-1060~~ 975-1060 of *E. coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;

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bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA;

bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;

bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;

bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;

bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA;

bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and

bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA,

provided that if said target region is ~~present~~ in a location corresponding to bases ~~1250-1290~~ 1255-1290 of *E. coli* 16S rRNA, or the encoding DNA, then said one or more target species is *Mycoplasma pneumoniae*; and

b) determining whether a nucleic acid complex comprising said oligonucleotide probe has formed under conditions of high stringency as an indication that at least one member of said one or more target species is present in said sample, wherein said oligonucleotide probe does not form a detectable duplex with nucleic acid of said at least one non-target species under said conditions.

490. (Currently Amended) A method for determining whether one or more non-viral target species may be present in a sample, said method comprising the steps of:

a) contacting said sample with hybridization assay means for detecting the presence of a nucleic acid variable region characteristic of nucleic acid of two or more non-viral target species belonging to a first genus, at least one of which is said one or more target species, wherein said means distinguishes said variable region from nucleic acid of at least one non-target species belonging to a second genus which is different from said first genus, wherein said variable region is present in an rRNA sequence, or a DNA sequence encoding for said rRNA sequence, in a location corresponding to a target region selected from the group consisting of:

bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;

bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;

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bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;

bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;

bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;

bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;

bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;

bases ~~980-1060~~ 975-1060 of *E. coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;

bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;

bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;

bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;

bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA;

bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and

bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA,

provided that if said target region is in a location corresponding to bases 975-1060 of *E. coli* 16S rRNA, or the encoding DNA, then said first genus is either *Campylobacter, Legionella,* or *Mycobacterium*; and

b)   determining whether said means has detected the presence of said variable region as an indication that at least one member of said one or more target species is present in said sample.

491.   (Currently Amended) A method for determining whether one or more non-viral target species may be present in a sample, said method comprising the steps of:

a)   contacting said sample with an oligonucleotide probe able to distinguish nucleic acid of two or more non-viral target species belonging to a first genus, at least one of which is said one or more target species, from nucleic acid of at least one non-viral non-target species belonging to a second genus, wherein a duplex formed between said oligonucleotide probe and a

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variable region present in nucleic acid of each of said two or more target species has a higher Tm than a duplex formed between said oligonucleotide probe and said variable region present in nucleic acid of said at least one non-target species, wherein said variable region is present in an rRNA sequence, or a DNA sequence encoding for said rRNA sequence, in a location corresponding to a target region selected from the group consisting of :

bases 65-108 of *E. coli* 5S rRNA or the encoding DNA;

bases 60-105 of *E. coli* 16S rRNA or the encoding DNA;

bases 120-150 of *E. coli* 16S rRNA or the encoding DNA;

bases 170-230 of *E. coli* 16S rRNA or the encoding DNA;

bases 405-490 of *E. coli* 16S rRNA or the encoding DNA;

bases 600-675 of *E. coli* 16S rRNA or the encoding DNA;

bases 705-735 of *E. coli* 16S rRNA or the encoding DNA;

bases 820-870 of *E. coli* 16S rRNA or the encoding DNA;

bases ~~980-1060~~ 975-1060 of *E. coli* 16S rRNA or the encoding DNA;

bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA;

bases 270-405 of *E. coli* 23S rRNA or the encoding DNA;

bases 535-575 of *E. coli* 23S rRNA or the encoding DNA;

bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA;

bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA;

bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA; and

bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA.

provided that if said target region is in a location corresponding to bases 975-1060 of *E. coli* 16S rRNA, or the encoding DNA, then said first genus is either *Campylobacter*, *Legionella*, or *Mycobacterium*; and

b)   determining whether a nucleic acid complex comprising said oligonucleotide probe has formed under conditions of high stringency as an indication that at least one member of said one or more target species is present in said sample, wherein said oligonucleotide probe does

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not form a detectable duplex with nucleic acid of said at least one non-target species under said conditions.

492.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 65-108 of *E. coli* 5S rRNA or the encoding DNA.

493.   (Previously Presented) The method of claim 492, wherein said target region is in a location corresponding to bases 65-108 of *E. coli* 5S rRNA.

494.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 60-100 of *E. coli* 16S rRNA or the encoding DNA.

495.   (Previously Presented) The method of claim 494, wherein said target region is in a location corresponding to bases 60-100 of *E. coli* 16S rRNA.

496.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 120-150 of *E. coli* 16S rRNA or the encoding DNA.

497.   (Previously Presented) The method of claim 496, wherein said target region is in a location corresponding to bases 120-150 of *E. coli* 16S rRNA.

498.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 170-230 of *E. coli* 16S rRNA or the encoding DNA.

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499.   (Previously Presented)   The method of claim 498, wherein said target region is in a location corresponding to bases 170-230 of *E. coli* 16S rRNA.

500.   (Previously Presented)   The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 405-480 of *E. coli* 16S rRNA or the encoding DNA.

501.   (Previously Presented)   The method of claim 500, wherein said target region is in a location corresponding to bases 405-480 of *E. coli* 16S rRNA.

502.   (Previously Presented)   The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 600-670 of *E. coli* 16S rRNA or the encoding DNA.

503.   (Previously Presented)   The method of claim 502, wherein said target region is in a location corresponding to bases 600-670 of *E. coli* 16S rRNA.

504.   (Previously Presented)   The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 705-735 of *E. coli* 16S rRNA or the encoding DNA.

505.   (Previously Presented)   The method of claim 504, wherein said target region is in a location corresponding to bases 705-735 of *E. coli* 16S rRNA.

506.   (Previously Presented)   The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 820-860 of *E. coli* 16S rRNA or the encoding DNA.

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507.   (Previously Presented) The method claim 506, wherein said target region is in a location corresponding to bases 820-860 of *E. coli* 16S rRNA.

508.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 980-1050 of *E. coli* 16S rRNA or the encoding DNA.

509.   (Previously Presented) The method of claim 508, wherein said target region is in a location corresponding to bases 980-1050 of *E. coli* 16S rRNA.

510.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA.

511.   (Previously Presented) The method of claim 510, wherein said target region is in a location corresponding to bases 1125-1155 of *E. coli* 16S rRNA.

512.   (Previously Presented) The method of any one of claims 486-489, wherein said target region is in a location corresponding to either bases 1250-1290 of *E. coli* 16S rRNA or the encoding DNA.

513.   (Previously Presented) The method of claim 512, wherein said target region is in a location corresponding to bases 1250-1290 of *E. coli* 16S rRNA.

514.   (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 270-390 of *E. coli* 23S rRNA or the encoding DNA.

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515. (Previously Presented) The method of claim 514, wherein said target region is in a location corresponding to bases 270-390 of *E. coli* 23S rRNA.

516. (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 535-560 of *E. coli* 23S rRNA or the encoding DNA.

517. (Previously Presented) The method of claim 516, wherein said target region is in a location corresponding to bases 535-560 of *E. coli* 23S rRNA.

518. (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA.

519. (Previously Presented) The method of claim 518, wherein said target region is in a location corresponding to bases 1150-1200 of *E. coli* 23S rRNA.

520. (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA.

521. (Previously Presented) The method of claim 520, wherein said target region is in a location corresponding to bases 1440-1600 of *E. coli* 23S rRNA.

522. (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA.

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523. (Previously Presented) The method of claim 522, wherein said target region is in a location corresponding to bases 1710-1750 of *E. coli* 23S rRNA.

524. (Previously Presented) The method of any one of claims 486-491, wherein said target region is in a location corresponding to either bases 2190-2330 of *E. coli* 23S rRNA or the encoding DNA.

525. (Previously Presented) The method of claim 524, wherein said target region is in a location corresponding to bases 2190-2330 of *E. coli* 23S rRNA.

526. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 65-108 of *E. coli* 5S rRNA or the encoding DNA and said genus is *Mycoplasma*.

527. (Previously Presented) The method of claim 526, wherein said target region is in a location corresponding to bases 65-108 of *E. coli* 5S rRNA.

528. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 60-105 of *E. coli* 16S rRNA or the encoding DNA and said genus is *Chlamydia*.

529. (Previously Presented) The method of claim 528, wherein said target region is in a location corresponding to bases 60-105 of *E. coli* 16S rRNA.

530. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 120-150 of *E. coli* 16S rRNA or the encoding DNA and said genus is *Neisseria*.

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531. (Previously Presented) The method of claim 530, wherein said target region is in a location corresponding to bases 120-150 of *E. coli* 16S rRNA.

532. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding either bases 170-230 of E. coli 16S rRNA or the encoding DNA and said genus is either *Mycobacterium*, *Chlamydia*, or *Mycoplasma*.

533. (Previously Presented) The method of claim 532, wherein said genus is *Mycobacterium* and said target region is in a location corresponding to either bases 185-225 of *E. coli* 16S rRNA or the encoding DNA.

534. (Previously Presented) The method of claim 533, wherein said target region is in a location corresponding to bases 185-225 of *E. coli* 16S rRNA.

535. (Previously Presented) The method of claim 532, wherein said genus is *Chlamydia* and said target region is in a location corresponding to either bases 175-210 of *E. coli* 16S rRNA or the encoding DNA.

536. (Previously Presented) The method of claim 535, wherein said target region is in a location corresponding to bases 175-210 of *E. coli* 16S rRNA.

537. (Previously Presented) The method of claim 532, wherein said genus is *Mycoplasma* and said target region is in a location corresponding to either bases 190-230 of *E. coli* 16S rRNA or the encoding DNA.

538. (Previously Presented) The method of claim 537, wherein said target region is in a location corresponding to bases 190-230 of *E. coli* 16S rRNA.

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539. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 405-490 of *E. coli* 16S rRNA or the encoding DNA and said genus is either *Mycoplasma* or *Neisseria*.

540. (Previously Presented) The method of claim 539, wherein said target region is in a location corresponding to bases 405-490 of *E. coli* 16S rRNA.

541. (Previously Presented) The method of claim 539, wherein said genus is *Mycoplasma* and said target region is in a location corresponding to either bases 450-490 of *E. coli* 16S rRNA or the encoding DNA.

542. (Previously Presented) The method of claim 541, wherein said target region is in a location corresponding to bases 450-490 of *E. coli* 16S rRNA.

543. (Previously Presented) The method of claim 539, wherein said genus is *Neisseria* and said target region is in a location corresponding to either bases 455-485 of *E. coli* 16S rRNA or the encoding DNA.

544. (Previously Presented) The method of claim 543, wherein said target region is in a location corresponding to bases 455-485 of *E. coli* 16S rRNA.

545. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 600-635 of *E. coli* 16S rRNA or the encoding DNA and said genus is *Chlamydia*.

546. (Previously Presented) The method of claim 545, wherein said target region is in a location corresponding to bases 600-635 of *E. coli* 16S rRNA.

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547.   (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 820-870 of *E. coli* 16S rRNA or the encoding DNA and said genus is either *Chlamydia, Mycoplasma,* or *Streptococcus.*

548.   (Previously Presented) The method of claim 547, wherein said target region is in a location corresponding to bases 820-870 of *E. coli* 16S rRNA.

549.   (Previously Presented) The method of claim 547, wherein said genus is *Chlamydia* and said target region is in a location corresponding to either bases 830-870 of *E. coli* 16S rRNA or the encoding DNA.

550.   (Previously Presented) The method of claim 549, wherein said target region is in a location corresponding to bases 830-870 of *E. coli* 16S rRNA.

551.   (Previously Presented) The method of claim 547, wherein said genus is *Mycoplasma* and said target region is in a location corresponding to either bases 820-860 of *E. coli* 16S rRNA or the encoding DNA.

552.   (Previously Presented) The method of claim 551, wherein said target region is in a location corresponding to bases 820-860 of *E. coli* 16S rRNA.

553.   (Previously Presented) The method of claim 547, wherein said genus is *Streptococcus* and said target region is in a location corresponding to either bases 825-860 of *E. coli* 16S rRNA or the encoding DNA.

554.   (Previously Presented) The method of claim 553, wherein said target region is in a location corresponding to bases 825-860 of *E. coli* 16S rRNA.

555.   (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 980-1050 of E. coli 16S rRNA or the encoding DNA and said genus is either *Escherichia* or *Neisseria*.

556.   (Previously Presented) The method of claim 555, wherein said target region is in a location corresponding to bases 980-1050 of *E. coli* 16S rRNA.

557.   (Previously Presented) The method of claim 555, wherein said genus is *Escherichia* and said target region is in a location corresponding to either bases 995-1030 of *E. coli* 16S rRNA or the encoding DNA.

558.   (Previously Presented) The method of claim 557, wherein said target region is in a location corresponding to bases 995-1030 of *E. coli* 16S rRNA.

559.   (Previously Presented) The method of claim 555, wherein said genus is *Neisseria* and said target region is in a location corresponding to either bases 980-1015 of *E. coli* 16S rRNA or the encoding DNA.

560.   (Previously Presented) The method of claim 559, wherein said target region is in a location corresponding to bases 980-1015 of *E. coli* 16S rRNA.

561.   Canceled

562.   Canceled

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563. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 270-405 of *E. coli* 23S rRNA or the encoding DNA and said genus is either *Chlamydia, Proteus, Pseudomonas,* or *Enterobacter.*

564. (Previously Presented) The method of claim 563, wherein said target region is in a location corresponding to bases 270-405 of *E. coli* 23S rRNA.

565. (Previously Presented) The method of claim 563, wherein said genus is *Chlamydia* and said target region is in a location corresponding to either bases 275-320 of *E. coli* 23S rRNA or the encoding DNA.

566. (Previously Presented) The method of claim 565, wherein said target region is in a location corresponding to bases 275-320 of *E. coli* 23S rRNA.

567. (Previously Presented) The method of claim 563, wherein said genus is *Chlamydia* and said target region is in a location corresponding to either bases 330-365 of *E. coli* 23S rRNA or the encoding DNA.

568. (Previously Presented) The method of claim 567, wherein said target region is in a location corresponding to bases 330-365 of *E. coli* 23S rRNA.

569. (Previously Presented) The method of claim 563, wherein said genus is *Proteus* and said target region is in a location corresponding to either bases 270-305 of *E. coli* 23S rRNA or the encoding DNA.

570. (Previously Presented) The method of claim 569, wherein said target region is in a location corresponding to bases 270-305 of *E. coli* 23S rRNA.

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571. (Previously Presented) The method of claim 563, wherein said genus is *Pseudomonas* and said target region is in a location corresponding to either bases 365-405 of *E. coli* 23S rRNA or the encoding DNA.

572. (Previously Presented) The method of claim 571, wherein said target region is in a location corresponding to bases 365-405 of *E. coli* 23S rRNA.

573. (Previously Presented) The method of claim 563, wherein said genus is *Enterobacter* and said target region is in a location corresponding to either bases 305-340 of *E. coli* 23S rRNA or the encoding DNA.

574. (Previously Presented) The method of claim 573, wherein said target region is in a location corresponding to bases 305-340 of *E. coli* 23S rRNA.

575. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 540-575 of *E. coli* 23S rRNA or the encoding DNA and said genus is *Mycobacterium*.

576. (Previously Presented) The method of claim 575, wherein said target region is in a location corresponding to bases 540-575 of *E. coli* 23S rRNA.

577. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 1150-1200 of *E. coli* 23S rRNA or the encoding DNA and said genus is either *Mycobacterium* or *Chlamydia*.

578. (Previously Presented) The method of claim 577, wherein said target region is in a location corresponding to bases 1150-1200 of *E. coli* 23S rRNA.

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579. (Previously Presented) The method of claim 578, wherein said genus is *Mycobacterium* and said target region is in a location corresponding to either bases 1155-1190 of *E. coli* 23S rRNA or the encoding DNA.

580. (Previously Presented) The method of claim 579, wherein said target region is in a location corresponding to bases 1155-1190 of *E. coli* 23S rRNA.

581. (Previously Presented) The method of claim 577, wherein said genus is *Chlamydia* and said target region is in a location corresponding to either bases 1160-1190 of *E. coli* 23S rRNA or the encoding DNA.

582. (Previously Presented) The method of claim 581, wherein said target region is in a location corresponding to bases 1160-1190 of *E. coli* 23S rRNA.

583. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 1440-1600 of *E. coli* 23S rRNA or the encoding DNA and said genus is *Chlamydia*.

584. (Previously Presented) The method of claim 583, wherein said target region is in a location corresponding to bases 1440-1600 of *E. coli* 23S rRNA.

585. (Previously Presented) The method of claim 583, wherein said target region is in a location corresponding to either bases 1450-1490 of *E. coli* 23S rRNA or the encoding DNA.

586. (Previously Presented) The method of claim 585, wherein said target region is in a location corresponding to bases 1450-1490 of *E. coli* 23S rRNA.

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587. (Previously Presented) The method of claim 583, wherein said target region is in a location corresponding to either bases 1510-1545 of *E. coli* 23S rRNA or the encoding DNA.

588. (Previously Presented) The method of claim 587, wherein said target region is in a location corresponding to bases 1510-1545 of *E. coli* 23S rRNA.

589. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 1710-1750 of *E. coli* 23S rRNA or the encoding DNA and said genus is *Chlamydia.*

590. (Previously Presented) The method of claim 589, wherein said target region is in a location corresponding to bases 1710-1750 of *E. coli* 23S rRNA.

591. (Previously Presented) The method of claim 488 or 489, wherein said target region is in a location corresponding to either bases 2195-2235 of *E. coli* 23S rRNA or the encoding DNA and said genus is *Mycobacterium.*

592. (Previously Presented) The method of claim 591, wherein said target region is in a location corresponding to bases 2195-2235 of *E. coli* 23S rRNA.

593. (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 405-480 of *E. coli* 16S rRNA or the encoding DNA and said first genus is *Campylobacter.*

594. (Previously Presented) The method of claim 593, wherein said target region is in a location corresponding to bases 405-480 of *E. coli* 16S rRNA.

595. (Previously Presented) The method of claim 593, wherein said target region is in a location corresponding to either bases 405-428 of *E. coli* 16S rRNA or the encoding DNA.

596. (Previously Presented) The method of claim 595, wherein said target region is in a location corresponding to bases 405-428 of *E. coli* 16S rRNA.

597. (Previously Presented) The method of claim 593, wherein said target region is in a location corresponding to either bases 440-470 of *E. coli* 16S rRNA or the encoding DNA.

598. (Previously Presented) The method of claim 597, wherein said target region is in a location corresponding to bases 440-470 of *E. coli* 16S rRNA.

599. (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 630-675 of *E. coli* 16S rRNA or the encoding DNA and said first genus is *Legionella*.

600. (Previously Presented) The method of claim 599, wherein said target region is in a location corresponding to bases 630-675 of *E. coli* 16S rRNA.

601. (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 705-735 of *E. coli* 16S rRNA or the encoding DNA and said first genus is *Campylobacter*.

602. (Previously Presented) The method of claim 601, wherein said target region is in a location corresponding to bases 705-735 of *E. coli* 16S rRNA.

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603.   (Currently Amended) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 975-1060 of *E. coli* 16S rRNA or the encoding DNA ~~and said first genus is either Campylobacter, Legionella, or Mycobacterium.~~

604.   (Currently Amended) The method of claim 603, wherein said target region is in a location corresponding to bases ~~980-1060~~ 975-1060 of *E. coli* 16S rRNA.

605.   (Previously Presented) The method of claim 603, wherein said first genus is *Campylobacter* and said target region is in a location corresponding to either bases 980-1010 of *E. coli* 16S rRNA or the encoding DNA.

606.   (Previously Presented) The method of claim 605, wherein said target region is in a location corresponding to bases 980-1010 of *E. coli* 16S rRNA.

607.   (Previously Presented) The method of claim 603, wherein said first genus is *Legionella* and said target region is in a location corresponding to either bases 975-1020 of *E. coli* 16S rRNA or the encoding DNA.

608.   (Previously Presented) The method of claim 607, wherein said target region is in a location corresponding to bases 975-1020 of *E. coli* 16S rRNA.

609.   (Previously Presented) The method of claim 603, wherein said first genus is *Mycobacterium* and said target region is in a location corresponding to either bases 1025-1060 of *E. coli* 16S rRNA or the encoding DNA.

610.   (Previously Presented) The method of claim 609, wherein said target region is in a location corresponding to bases 1025-1060 of *E. coli* 16S rRNA.

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611.   (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 1125-1155 of *E. coli* 16S rRNA or the encoding DNA and said first genus is *Salmonella.*

612.   (Previously Presented) The method of claim 611, wherein said target region is in a location corresponding to bases 1125-1155 of *E. coli* 16S rRNA.

613.   (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 270-395 of *E. coli* 23S rRNA or the encoding DNA and said first genus is either *Legionella* or *Salmonella.*

614.   (Previously Presented) The method of claim 613, wherein said target region is in a location corresponding to bases 270-395 of *E. coli* 23S rRNA.

615.   (Previously Presented) The method of claim 613, wherein said first genus is *Legionella* and said target region is in a location corresponding to either bases 350-395 of *E. coli* 23S rRNA or the encoding DNA.

616.   (Previously Presented) The method of claim 615, wherein said target region is in a location corresponding to bases 350-395 of *E. coli* 23S rRNA.

617.   (Previously Presented) The method of claim 613, wherein said first genus is *Salmonella* and said target region is in a location corresponding to either bases 335-375 of *E. coli* 23S rRNA or the encoding DNA.

618.   (Previously Presented) The method of claim 617, wherein said target region is in a location corresponding to bases 335-375 of *E. coli* 23S rRNA.

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619. (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 1440-1620 of *E. coli* 23S rRNA or the encoding DNA and said first genus is either *Legionella* or *Mycobacterium*.

620. (Previously Presented) The method of claim 619, wherein said target region is in a location corresponding to bases 1440-1620 of *E. coli* 23S rRNA.

621. (Previously Presented) The method of claim 620, wherein said first genus is *Legionella* and said target region is in a location corresponding to either bases 1585-1620 of *E. coli* 23S rRNA or the encoding DNA.

622. (Previously Presented) The method of claim 621, wherein said target region is in a location corresponding to bases 1585-1620 of *E. coli* 23S rRNA.

623. (Previously Presented) The method of claim 619, wherein said first genus is *Mycobacterium* and said target region is in a location corresponding to either bases 1440-1475 of *E. coli* 23S rRNA or the encoding DNA.

624. (Previously Presented) The method of claim 623, wherein said target region is in a location corresponding to bases 1440-1475 of *E. coli* 23S rRNA.

625. (Previously Presented) The method of claim 619, wherein said first genus is *Mycobacterium* and said target region is in a location corresponding to either bases 1515-1555 of *E. coli* 23S rRNA or the encoding DNA.

626. (Previously Presented) The method of claim 625, wherein said target region is in a location corresponding to bases 1515-1555 of *E. coli* 23S rRNA.

627. (Previously Presented) The method of claim 619, wherein said first genus is *Mycobacterium* and said target region is in a location corresponding to either bases 1570-1610 of *E. coli* 23S rRNA or the encoding DNA.

628. (Previously Presented) The method of claim 627, wherein said target region is in a location corresponding to bases 1570-1610 of *E. coli* 23S rRNA.

629. (Previously Presented) The method of claim 490 or 491, wherein said target region is in a location corresponding to either bases 2280-2330 of *E. coli* 23S rRNA or the encoding DNA and said first genus is *Legionella*.

630. (Previously Presented) The method of claim 629, wherein said target region is in a location corresponding to bases 2280-2330 of *E. coli* 23S rRNA.